

SISG/SISMID Module 3

Introduction to R

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University of Washington

Seattle, July 2020

Introduction: Course Aims

This is a *first* course in R. We aim to cover;

- Reading in, summarizing & managing data
- Use of functions in R doing jobs by programming, not by using drop-down menus (much)
- Some standard functions for statistical analysis but minimal statistics in this module
- How to use other people's code, how to get help, what to learn next

We assume no previous use of R, also non-extensive programming skills in other languages. If this is *not* your level, please consider switching to a later module.

Introduction: Resources

Most importantly, the class site is

http://faculty.washington.edu/kenrice/rintro

Contains (or will contain);

- Links to all Zoom sessions, and their recordings
- PDF copies of slides (in color, and contains a few hyperlinks)
- All datasets needed for exercises
- Exercises for you to try
- Our solutions to exercises (later!)
- Links to other software, other courses, book, and places to get R help
- Links to a few helpful websites/email list archives

Of course, search engines will find much more than this, and can be a useful start, when tackling analyses with R.

Introduction: About Tim



- Professor, UW Biostat
- A useR and an instructoR
- Research in Genetic
 Epidemiology for Complex
 Human Traits

Introduction: About Ken



- Professor, UW Biostat
- Author of a few R packages, user, teacher
- Genetic/Genomic research in Cardiovascular Epidemiology

Introduction: Teaching Assistants

Our department's finest — here to help you:

Chloe Krakauer



Amarise Little



Yilin Song



Expect to 'see' them on Zoom chat, and our Slack channel.

Introduction: Course structure

10 sessions over 2.5 days

- Day 1; (Mostly RStudio) Data management, using functions
- Day 2; (Standard R) More about programming
- Day 2.5; More advanced ideas

Web page: http://faculty.washington.edu/kenrice/rintro/

Introduction: Session structure

What to expect in a typical 80 minute session;

- 45 mins teaching (please ask questions, on Zoom and/or Slack)
- 25 mins hands-on; in Zoom breakout rooms, please discuss as you go
- 10 mins summary, discussion/extensions (questions again!)

Please note: the 2.5 day course moves quickly, and later material builds on earlier material. So, **please ask questions!** – as 'chat' in Zoom calls, or on our Slack channel.



1. Reading in data

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What is R?

R is a 'programming environment for statistics and graphics'

- Does basically everything, can also be extended
- It's the default when statisticians implement new methods
- Free, open-source

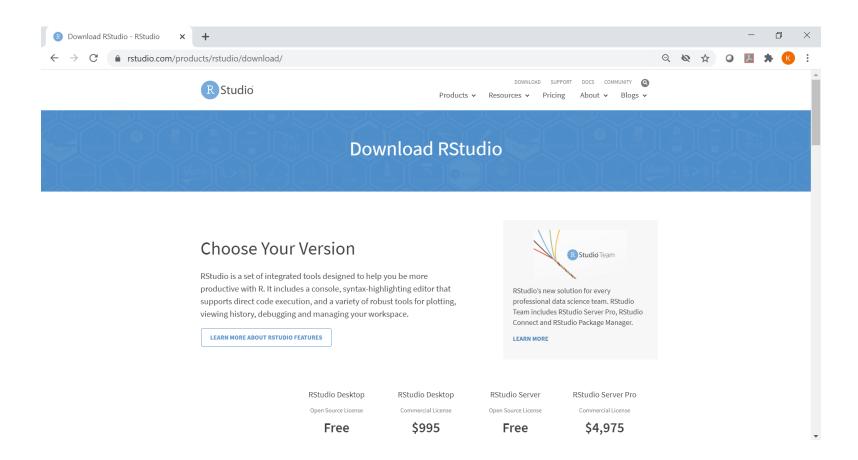
But;

- Steeper learning curve than e.g. Excel, Stata
- Command-line driven (programming, not drop-down menus)
- Gives only what you ask for!

To help with these difficulties, we will begin with RStudio, a graphical user interface (front-end) for R that is slightly more user-friendly than 'Classic' R's GUI.

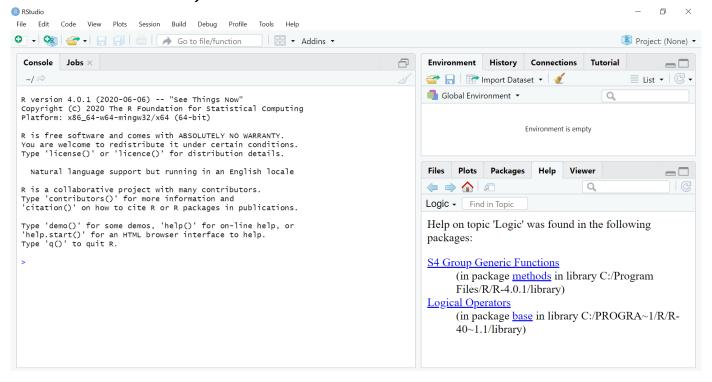
So after you have installed the latest version of R...

In your favorite web browser, download RStudio for Desktop;



- Select& download the FREE installer for your system
- Default installation is fine

RStudio is a 'front end' to R itself, so needs you to install R. On first startup, RStudio should look like this; (up to version and Mac/PC differences)



If you've used it before, RStudio defaults to remembering what you were doing.

We'll use the 'Console' window first — as a (fancy!) calculator

```
> 2+2
[1] 4
> 2^5+7
[1] 39
> 2^(5+7)
[1] 4096
> exp(pi)-pi
[1] 19.9991
> log(20+pi)
[1] 3.141632
> 0.05/1E6  # a comment; note 1E6 = 1,000,000
[1] 5e-08
```

- All common math functions are available; parentheses (round brackets) work as per high school math
- Try to get used to bracket matching. A '+' prompt means the line isn't finished – hit Escape to get out, then try again.

R stores data (and everything else) as *objects*. New objects are created when we *assign* them values;

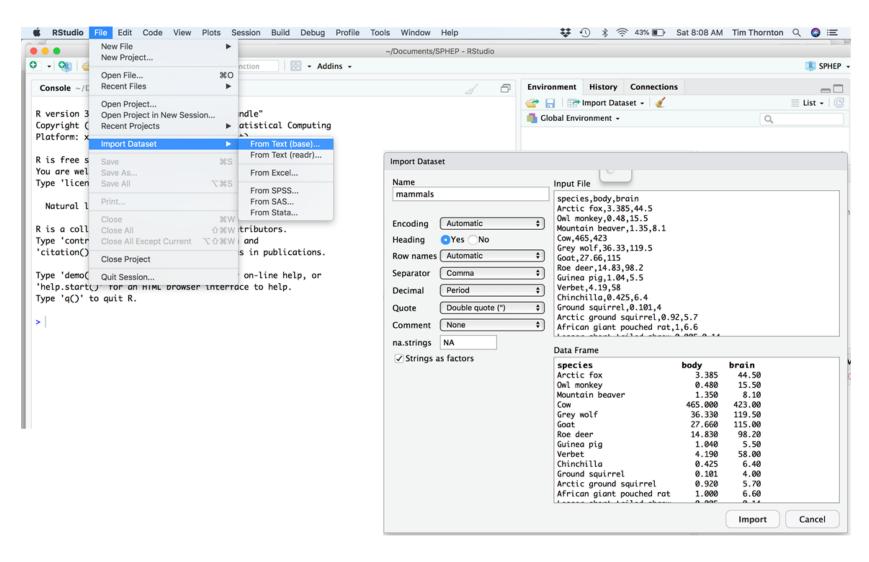
```
> x <- 3
> y <- 2 # now check the Environment window
> x+y
[1] 5
```

Assigning new values to existing objects over-writes the old version — and be aware there is no Ctrl-Z 'undo';

```
> y <- 17.4 # check the Environment window again > x+y [1] 20.4
```

- Anything after a hash (#) is ignored e.g. comments
- Spaces don't matter
- Capital letters do matter

To import a dataset, follow pop-ups from the File tab;



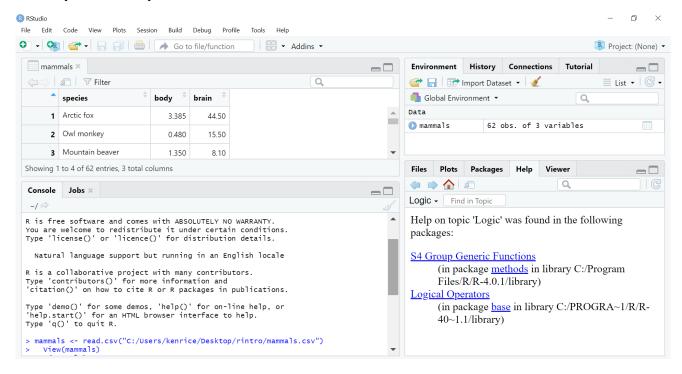
More on those options;

- Name: Name of the object that will store the whole dataset, when it's read in
- **Heading**: Does the first row contain column names?
- Row names: are there names for each row?
- **Separator**: what's between items on a single line?
- na.strings: How are missing values denoted?

The defaults are sensible, but R assumes you *know* what your data *should* look like — and whether it has named columns, numeric/character data, etc. *No* software is smart enough to cope with every format that might be used by you/your colleagues to store data.

After successfully reading in the data;

- The environment now includes a mammals object or whatever you called the data read from file
- A copy of the data can be examined in the Excel-like data viewer (below) – if it looks weird, find out why & fix it!



... we'll return later, to read.csv() in the Console window

What's a good name for my new object?

- Something memorable (!) and not easily-confused with other objects, e.g. X isn't a good choice if you already have x
- Names must start with a letter or period ("."), after that any letter, number or period is okay
- Avoid other characters; they get interpreted as math
 ("-","*") or are hard to read ("_") so should not be used in
 names
- Avoid names of existing functions e.g. summary. Some oneletter choices (c, C, F, t, T and S) are already used by R as names of functions, it's best to avoid these too

Operating on data

To operate on data, type commands in the Console window, just like our earlier calculator-style approach;

```
> str(mammals)
'data.frame': 62 obs. of 3 variables:
$ species: chr "Arctic fox" "Owl monkey" "Mountain beaver" "Cow" ...
$ body : num 3.38 0.48 1.35 465 36.33 ...
$ brain : num 44.5 15.5 8.1 423 119.5 ...
> summary(mammals)
  species
                                       brain
                      body
Length:62
                 Min. : 0.005 Min. : 0.14
Class: character 1st Qu.: 0.600 1st Qu.: 4.25
Mode : character Median : 3.342
                                   Median: 17.25
                  Mean : 198.790 Mean : 283.13
                  3rd Qu.: 48.202 3rd Qu.: 166.00
                  Max. :6654.000 Max. :5712.00
```

- str() tells us the structure of an object
- summary() summarizes the object

Can also use these commands on any object — e.g. the single numbers we created earlier (try it!)

Operating on data: columns

Individual columns in data frames are identified using the \$ symbol – just seen in the str() output.

```
> mammals$brain
 [1]
     44.50
                 8.10 423.00
                                119.50 115.00
                                               98.20
            15.50
                                                      5.50
                                                            58.00
Γ10]
      6.40
                    5.70
                           6.60
                                               10.80
           4.00
                                  0.14
                                         1.00
                                                     12.30
                                                             6.30
[19] 4603.00
           0.30 419.00 655.00
                                               25.60
                                  3.50 115.00
                                                    5.00
                                                            17.50
[28] 680.00 406.00 325.00 12.30 1320.00 5712.00
                                              3.90
                                                    179.00 56.00
[37] 17.00
           1.00 0.40 0.25
                               12.50 490.00
                                              12.10
                                                    175.00
                                                            157.00
[46] 440.00
           179.50 2.40 81.00 21.00 39.20 1.90 1.20
                                                             3.00
[55] 0.33
           180.00 25.00 169.00 2.60 11.40 2.50 50.40
> summary(mammals$brain)
  Min. 1st Qu. Median Mean 3rd Qu.
                                    Max.
         4.25 17.25 283.10 166.00 5712.00
  0.14
```

Think of \$ as 'apostrophe-S', i.e. mammals'S brain.

Unlike many other statistical packages, R can handle *multiple* datasets at the same time — helpful if your data are e.g. phenotypes & genotypes, or county & disease outbreak data. This isn't possible without \$, or *some* equivalent syntax.

Operating on data: columns

New columns are created when you assign their values — here containing the brain weights in kilograms;

```
> mammals$brainkg <- mammals$brain/1000
> str(mammals)
'data.frame': 62 obs. of 4 variables:
   $ species: chr "Arctic fox" "Owl monkey" "Mountain beaver" "Cow" ...
   $ body : num     3.38     0.48     1.35     465     36.33 ...
   $ brain : num     44.5     15.5     8.1     423     119.5 ...
   $ brainkg: num     0.0445     0.0155     0.0081     0.423     0.1195 ...
> str(mammals$brainkg)
   num [1:62]     0.0445     0.0155     0.0081     0.423     0.1195 ...
> mammals$brainkg <- NULL</pre>
```

- Assigning values to existing columns over-writes existing values – again, with no warning
- With e.g. mammals\$newcolumn <- 0, the new column has every entry zero; R recycles this single value, for every entry
- It's unusual to delete columns... but if you *must*; mammals\$brainkg <- NULL

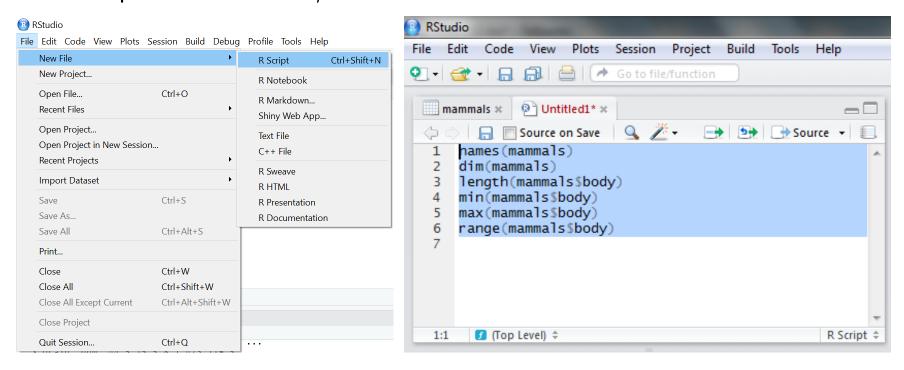
Operating on data: columns

Some other functions useful for summarizing data frames, and their columns;

```
> names(mammals)
[1] "species" "body" "brain"
> dim(mammals)  # dim is short for dimension
[1] 62 3
> length(mammals$body) # how many rows in our dataset?
[1] 62
> min(mammals$body)
[1] 0.005
> max(mammals$body)
「1] 6654
> range(mammals$body)
[1] 0.005 6654.000
> mean(mammals$brain)
[1] 283.1342
> sd(mammals$brain) # sd is short for standard deviation
[1] 930.2789
> median(mammals$brain)
[1] 17.25
```

RStudio: the Script window

While fine for occasional use, entering *every* command 'by hand' is error-prone, and quickly gets tedious. A *much* better approach is to use a Script window – open one with Ctrl-Shift-N, or the drop-down menus;



- Opens a nice editor, enables saving code (.R extension)
- Run current line (or selected lines) with Ctrl-Enter, or Ctrl-R

RStudio: the Script window

An important notice: from now on, we assume you are using a script editor.

- First-time users tend to be reluctant to switch! but it's worth it, ask any experienced user
- Some code in slides may be formatted for cut-and-paste into scripts – it may not look exactly like what appears in the Console window
- Exercise 'solutions' given as .R files
- Scripts make it easy to run slightly modified code, without re-typing everything remember to save them as you work
- Also remember the Escape key, if e.g. your bracket-matching goes wrong

For a very few jobs, e.g. changing directories, we'll still use drop-down menus. But commands *are* available, for all tasks.

To identify general subsets – not just the columns selected by \$ – R uses square brackets. Selecting individuals elements;

```
> mammals$brain[32] # 32nd element of mammals$brain
[1] 1320
> mammals$species[32]
[1] "Human"
> mammals$body[32]
[1] 62
```

Can also select entire columns or entire rows this way — and 'blank' entries indicate you want everything.

```
> mammals[32,2] # subtable with just 32nd row, 2nd column
[1] 62
> mammals[32,] # everything in the 32nd row
    species body brain
32    Human 62 1320
> sum(mammals[,3]) # sum of all the brains masses...
[1] 17554.32
```

Suppose we were interested in the body weight (i.e. 2nd column) for mammals (i.e. rows) 14, 55, & 61. How to select these multiple elements?

```
> mammals[c(14,55,61),2]
[1] 0.005 0.048 0.104
```

But what is c(14,55,61)? It's a *vector* of numbers – c() is for *combine*;

```
> length(c(14,55,61))
[1] 3
> str(c(14,55,61))
num [1:3] 14 55 61
```

We can select these rows and all the columns;

A very useful special form of vector;

```
> 1:10
[1] 1 2 3 4 5 6 7 8 9 10
> 6:2
[1] 6 5 4 3 2
> -1:-3
[1] -1 -2 -3
```

R expects you know this shorthand — see e.g. its use of 1:3 in the output from str(), on the previous slide. For a 'rectangular' selection of rows and columns;

Negative values correspond to dropping those rows/columns;

```
> mammals[-3:-62, c(1,3)] # everything but the first two rows, & columns c(1,3)
        species brain
1 Arctic fox 44.5
2 Owl monkey 15.5
```

As well as storing numbers and character strings (like "Donkey", "Big brown bat") R can also store *logicals* — TRUE and FALSE.

To make a new vector, with elements that are TRUE if body mass is above 500kg and FALSE otherwise;

```
> is.heavy <- mammals$body > 500
> table(is.heavy) # another useful data summary command
is.heavy
     TRUE
FALSE
  58
         4
Which mammals were these? (And what were their masses?)
> mammals[is.heavy,] # just the rows for which is.heavy is TRUE
           species body brain
    Asian elephant 2547 4603
19
             Horse 521
22
                       655
           Giraffe 529 680
28
33 African elephant 6654 5712
```

Use e.g. mammals[is.heavy,2] to combine TRUE/FALSE (rows) and numbers (columns)

One final method... for now! Instead of specifying columns of interest by number, or through vectors of TRUEs/FALSEs, we can also just give the names – as *character strings*, or vectors of character strings.

```
> mammals[1:3, "body"]
[1] 3.385 0.480 1.350
> mammals[is.heavy,"body"]
[1] 2547 521 529 6654
```

this is more typing than the other methods, but is much easier to debug/reuse. Neither is 'right' or 'wrong' - R is just flexible.

Quitting time (almost)

When you're finished with RStudio;

- \bullet Ctrl-Q, or the drop-down menus, or entering q() at the command line all start the exit process
- You will be asked "Save workspace image to \sim /.RData?"
 - No/Don't Save: nothing is saved, and is not available when you re-start. This is recommended, because you will do different things in each session
 - Yes: Everything in memory is stored in R's internal format (.Rdata) and will be available when you re-start RStudio
 - Cancel: don't quit, go back
- Writing about what you did (output from a script) often takes much longer than re-running that script's analyses – so often, a 'commented' script is all the R you need to store

To get rid of *objects* in your current session, use rm(), e.g. rm(is.heavy, mammals, x, y) ... or RStudio's 'broom' button.

Summary

- In RStudio, read in data from the pop-up menu in the Environment window (or Tools menu)
- Data frames store data; can have many of these objects and multiple other objects, too
- Identify vectors with \$, subsets with square brackets
- Many useful summary functions are available, with sensible names
- Scripts are an important drudgery-avoidance tool!